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GENETIC VARIATION OF DOUGLAS-FIR IN THE NORTHERN ROCKY MOUNTAINS

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ABSTRACT

*Seven half-sib families from each of 24 populations were compared to assess genetic variation in 2-year height of Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings. Families from *Pseudotsuga menziesii*-*Calamagrostis rubescens* and *Abies lasiocarpa*-*Pachistima myrsinites* habitat types had lower mean heights than those from four other habitat types. Families from western Montana had lower mean heights than those from northern Idaho and eastern Washington, regardless of the habitat type and elevation of the seed source. Thirteen percent of the total variance was attributable to variation among half-sib families within populations.*

Adaptive genetic variation among populations develops through selection by natural environments. Thus, genetic variation may accumulate in species, such as Rocky Mountain Douglas-fir (*Pseudotsuga menziesii* var. *glauca*), that occur across broad environmental spectra. Environmental heterogeneity in the northern Rockies is partially discernible in terms of habitat types developed for northern Idaho and eastern Washington (Daubenmire and Daubenmire 1968) and for western Montana by Pfister and others (reports being reviewed). In both areas, Douglas-fir occurs across a broad range of environmental conditions: from the relatively low and dry sites on which Douglas-fir is climax, through the moist sites dominated by western redcedar and western hemlock, to the relatively cold sites dominated by subalpine fir. Ample opportunity exists for development of adaptive variation in Douglas-fir of the northern Rockies.

Previous studies have shown that within a particular locality, populations of Rocky mountain Douglas-fir were not differentiated according to contrasting microclimates associated with north or south aspects at elevations from 950 to 1,300 m. Nevertheless, relatively large proportions of genetic variance were associated with populations and families within populations (Rehfeldt 1974). Genetic variation on a larger geographic scale is further explored in the present study of Rocky Mountain Douglas-fir.

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MATERIALS AND METHODS

Cones were collected from seven trees in each of 24 populations (table 1) located within the area bounded by the Canadian border, the Columbia River, the Salmon River, and the Continental Divide. Four populations represented each of six habitats: (1) DF/Phma² = *Pseudotsuga menziesii*-*Physocarpus malvaceus* and DF/Syal = *Pseudotsuga menziesii*-*Symphoricarpos albus*, (2) DF/Caru = *Pseudotsuga menziesii*-*Calamagrostis rubescens*, (3) GF/Pamy = *Abies grandis*-*Pachistima myrsinites*, (4) WRC/Pamy = *Thuja plicata*-*Pachistima myrsinites*, (5) WH/Pamy = *Thuja plicata*-*Pachistima myrsinites*, and (6) AF/Pamy = *Abies lasiocarpa*-*Pachistima myrsinites*. DF/Phma and DF/Syal habitats were grouped because both represent relatively dry sites at relatively low elevations on which Douglas-fir is climax. An attempt was made to maximize geographic distances and elevational differences among populations representing the same habitat type.

Seeds were sown in a randomized complete block design consisting of two replicates at the USDA Forest Service Nursery at Coeur d'Alene, Idaho. In 1973, heights of the tallest 2-year-old trees within each sixth of each plot were measured. An analysis of variance (table 2) for a hierarchical model of random effects (Steel and Torrie 1960) was made on the original measurements.

Table 1.--Location, physiographic setting, and mean height of seedlings for each population

Population	Latitude	Longitude	Nearest community	Habitat type	Elevation	Mean height
					m	cm
1	48°55'	116°20'	Copeland, Idaho	DF/Phma	594	29.3
2	48°50'	114°50'	Eureka, Mont.	DF/Syal	1,116	23.4
3	47°35'	116°40'	Coeur d'Alene, Idaho	DF/Phma	701	27.4
4	46°05'	114°15'	Darby, Mont.	DF/Syal	1,280	20.6
5	48°40'	118°20'	Kettle Falls, Wash.	DF/Caru	1,219	21.9
6	48°10'	115°30'	Libby, Mont.	DF/Caru	1,753	13.7
7	46°50'	113°25'	Greenough, Mont.	DF/Caru	1,875	19.3
8	45°45'	114°30'	West Fork RD, Mont.	DF/Caru	1,875	13.9
9	48°00'	116°55'	Spirit Lake, Idaho	GF/Pamy	780	30.5
10	47°55'	114°00'	Bigfork, Mont.	GF/Pamy	975	27.2
11	45°45'	116°00'	Grangeville, Idaho	GF/Pamy	1,463	28.0
12	47°10'	114°35'	Stark, Mont.	GF/Pamy	1,158	20.2
13	48°40'	117°35'	Alladin, Wash.	WRC/Pamy	1,158	24.9
14	48°20'	116°15'	Hope, Idaho	WRC/Pamy	1,265	25.4
15	46°30'	115°50'	Pierce, Idaho	AF/Pamy	1,000	15.8
16	47°30'	113°35'	Seeley Lake, Mont.	WRC/Pamy	1,390	23.5
17	48°20'	116°50'	Coolin, Idaho	WH/Pamy	975	30.6
18	48°35'	115°20'	Warland, Mont.	WH/Pamy	1,128	26.3
19	47°00'	116°10'	Clarkia, Idaho	WH/Pamy	1,143	26.7
20	47°40'	115°10'	Thompson Falls, Mont.	WH/Pamy	1,109	25.9
21	48°15'	117°35'	Chewelah, Wash.	AF/Pamy	1,676	15.3
22	48°25'	114°35'	Whitefish, Mont.	AF/Pamy	1,091	20.8
23	47°30'	115°40'	Burke, Idaho	AF/Pamy	1,356	20.9
24	46°30'	115°00'	Powell, Idaho	WRC/Pamy	875	28.8

²Abbreviations preceding formal nomenclature for habitat types will be used in the remainder of this paper.

Table 2.--Form and results of analysis of variance of 2-year height

Source of variance	Degrees of freedom	Unweighted components expected in each mean square	Intraclass correlation
Replication	1	$\sigma_E^2 + \sigma_{RF}^2 + \sigma_R^2$	25.2**
Families	167	$\sigma_E^2 + \sigma_{RF}^2 + \sigma_F^2$	46.0**

Habitat types ^{1/}	5	$\sigma_E^2 + \sigma_{RF}^2 + \sigma_{F/P/H}^2 + \sigma_{P/H}^2 + \sigma_H^2$	15.4**
Populations within habitats ^{1/}	18	$\sigma_E^2 + \sigma_{RF}^2 + \sigma_{F/P/H}^2 + \sigma_{P/H}^2$	17.2**
Families within populations ^{1/}	144	$\sigma_E^2 + \sigma_{RF}^2 + \sigma_{F/P/H}^2$	13.5**

Replication X Families	167	$\sigma_E^2 + \sigma_{RF}^2$	17.0**
Error	1,638	σ_E^2	11.9

^{1/}Subdivisions of the effects of families.

** Statistical significance of *F* values at the 1 percent level of probability.

RESULTS AND DISCUSSION

Forty-six percent of the total variance in seedling height was associated with half-sib families (table 2). Effects of habitat types, populations within habitat types, and families within populations contributed nearly equally to the family variance. Thus, substantial proportions of genetic variance occur for each level of classification.

Effects of habitat types resulted primarily from low mean heights of seedlings representing DF/Caru and AF/Pamy types as shown in the following tabulation:

Habitat type	Height cm
DF/Phma and Syal	25.2
GF/Pamy	26.5
WRC/Pamy	25.7
WH/Pamy	27.4
DF/Caru	17.2
AF/Pamy	18.2

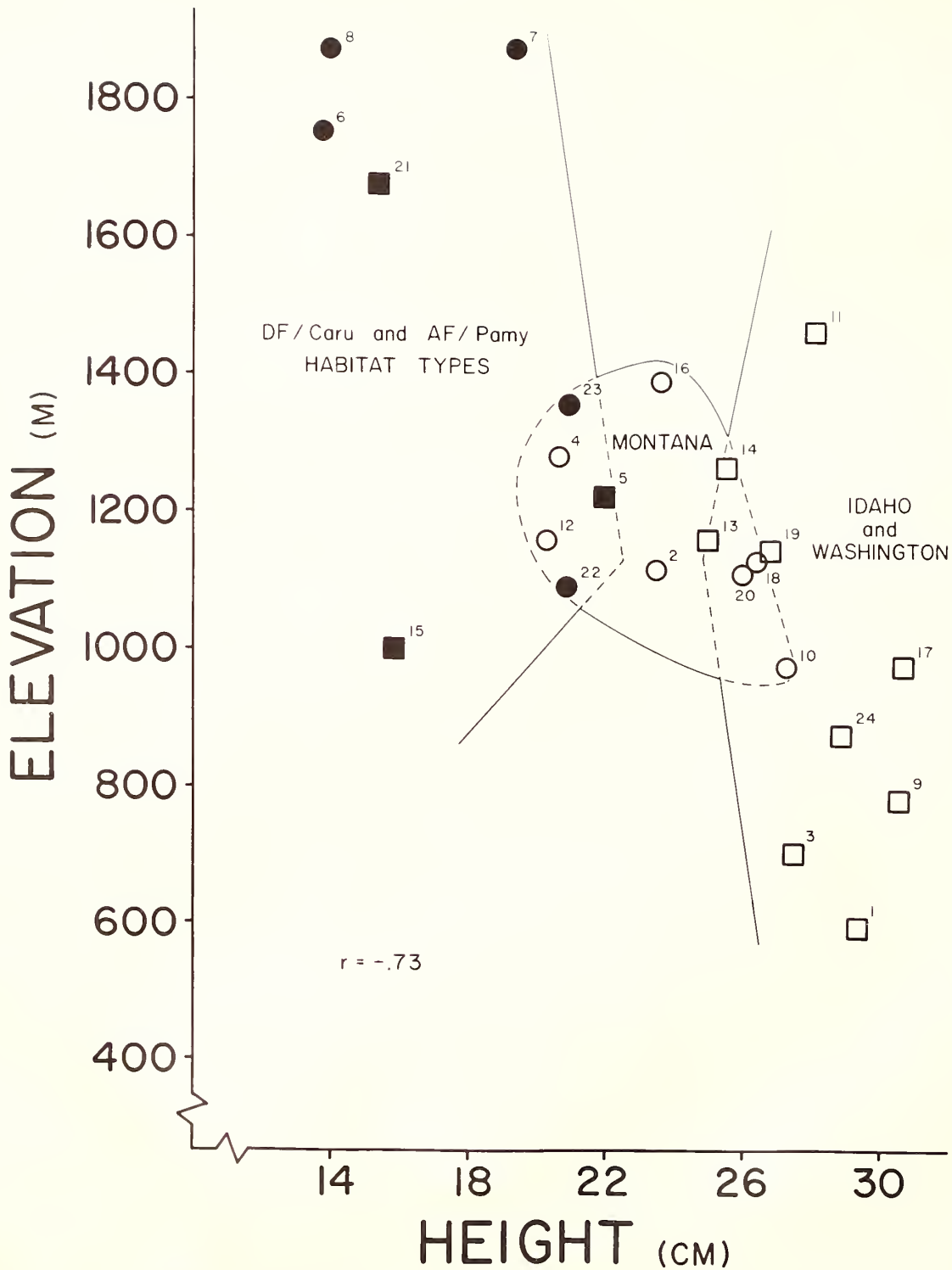


Figure 1.--Relationship between 2-year height of progenies and elevation of their origin. Square symbols = Idaho and Washington populations; round symbols = Montana populations; solid symbols = DF/Caru and AF/Pamy habitats. Numbers coding each population are keyed to Table 1.

Mean heights of seedlings from these two habitat types were significantly lower (5 percent level of probability) than those of seedlings from all other habitat types when the "S" test for multiple mean comparisons (Scheffé 1958) was applied. Evidently, pressures of selection associated with relatively cool DF/Caru and AF/Pamy habitats deviate sufficiently from those of other habitats to cause genetic differentiation.

Large effects for populations indicate that genetic differentiation is not solely interpretable in terms of habitat types. Indeed, the six populations of greatest mean seedling height were from Idaho (table 1). Scheffé's "S" test indicated significantly greater (5 percent level) mean heights associated with the group of populations from northern Idaho and eastern Washington than for those from western Montana, whether or not populations representing DF/Caru and AF/Pamy habitat types were excluded from the analysis. Differences between families from Idaho and those from Montana were also apparent in progeny tests conducted in the Midwest (Wright and others 1971). Evidently, the crests of the Bitterroot and Cabinet Mountains divide areas of contrasting selection pressures.

Mean heights of seedlings from each population and elevation where the populations occurred showed a significant ($r = -0.73$, 1 percent level) correlation (fig. 1). Although significant correlations between seedling height and elevation of the seed source are not uncommon (Roche 1969), the correlation observed with Douglas-fir is interpretable ecologically. In general, populations representing DF/Caru and AF/Pamy habitat types were from the highest elevations but were associated with the lowest mean heights. However, populations 15 and 22 represented the AF/Pamy habitat type in frost pockets at relatively low elevations; yet the mean height of families from these populations was similar to that of populations from AF/Pamy and DF/Caru habitats at the high elevations. Differentiation of populations from these habitat types appears to be a function of the cool environment associated with the habitat.

When the eight populations from DF/Caru and AF/Pamy habitat types are eliminated from the correlation procedure, the coefficient is reduced to -0.57 (significant at the 5 percent level). However, on the average, Montana populations had shorter families but were from higher elevations than those from Idaho and Washington. That differentiation of these groups is related to geography rather than elevation is suggested by the height of progenies from population 11; this Idaho population was from a relatively high elevation, but the mean height of its families was similar to that of families from Idaho and Washington (fig. 1). Moreover, significant correlations between height of families and elevation of the seed source were not observed within either the Montana or the Idaho and Washington groups. Differentiation appears to be related to geographic and ecologic factors which are intercorrelated with the elevation of the seed source.

Definition of large proportions of genetic variance for Rocky Mountain Douglas-fir can serve as a guide to forest management. The combination of these results with those suggesting a lack of local variation associated with aspect and elevation (Rehfeldt 1974) implies a minimum of three seed zones for the region under study: (1) DF/Caru and AF/Pamy habitat types, (2) western Montana, excluding DF/Caru and AF/Pamy habitats, and (3) northern Idaho and eastern Washington, excluding DF/Caru and AF/Pamy habitats. These three groupings collectively account for approximately 54 percent of the genetic variance. However, three seed zones are minimal; they are recommended on the basis of only one study conducted in only one environment for only one trait. Final definition of seed zones must be based on analyses of traits that depict the fitness of populations in a variety of natural environments.

Gains in productivity by means of tree breeding result from selective utilization of the genetic variance among families. Although 46 percent of the total variance was attributable to half-sib families, this value does not accurately estimate the half-sib component of variance because: (1) the progeny test was conducted in only one environment and, therefore, estimated components contain effects due to interaction between genotype

and environment; (2) only the tallest trees were measured within each plot and, therefore, error variances are probably underestimated; and (3) late spring frosts in 1973 caused substantial injury to developing buds on seedlings from certain families and populations. Although seedlings exhibiting pronounced effects of frost were not measured, differential injury nonetheless caused inflation of components of variance for half-sib families. For these reasons, the component of variance for families within populations (table 2) presumably estimates most accurately the half-sib component. The intraclass correlation for this effect was about 13 percent, a value that corresponds almost precisely to previous results (Rehfeldt 1974). Thus, 13 percent of the total variance is available for tree improvement; substantial proportions of additive genetic variance occur within Douglas-fir of the northern Rocky Mountains.

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LITERATURE CITED

- Daubenmire, R., and J. B. Daubenmire
1968. Forest vegetation of eastern Washington and northern Idaho. Wash. Agric. Ext. Stn. Tech. Bull. 60.
- Rehfeldt, G. E.
In press. Differentiation of populations of rocky Mountain Douglas-fir. Can. J. For. Res.
- Roche, L.
1969. A genealogical study of the genus *Picea* in British Columbia. New Phytol. 68:505-554.
- Scheffé, H.
1958. The analysis of variance. John Wiley, N.Y.
- Steel, R. G. D., and J. H. Torrie
1960. Principles and procedures of statistics. McGraw-Hill, N.Y.
- Wright, J. W., F. H. King, R. A. Read, W. A. Lemmien, and J. N. Bright
1971. Genetic variation in Rocky Mountain Douglas-fir. *Silvae Genet.* 20:54-60.

